

SEQUENCE LISTING

<110> Unilever plc

Unilever NV

<120> Production of Antibodies

<130> T7060

<160> 67

<170> PatentIn version 3.0

<210> 1

<211> 440

<212> DNA

<213> Artificial

<220>

<223> VHH with peptide linker

<220>

<221> CDS

<222> (1)..(417)

<400> 1

cag	gtg	cag	ctg	cag	gag	tca	ggg	gga	gga	ttg	gtg	cag	gct	ggg	ggc	48
Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Gly	
1			5						10					15		

tct	ctg	aga	ctc	toc	tgt	gca	gcc	tcg	gga	cgc	gcc	acc	agt	ggt	cat	96
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Ala	Thr	Ser	Gly	His	
		20						25					30			

ggt	cac	tat	ggt	atg	ggc	tgg	ttc	cgc	cag	gtt	cca	ggg	aag	gag	cgt	144
Gly	His	Tyr	Gly	Met	Gly	Trp	Phe	Arg	Gln	Val	Pro	Gly	Lys	Glu	Arg	
		35				40					45					

gag	ttt	gtc	gca	gct	att	agg	tgg	agt	ggt	aaa	gag	aca	tgg	tat	aaa	192
Glu	Phe	Val	Ala	Ala	Ile	Arg	Trp	Ser	Gly	Lys	Glu	Thr	Trp	Tyr	Lys	
	50				55						60					

gac	tcc	gtg	aag	ggc	cga	ttc	acc	atc	tcc	aga	gat	aac	gcc	aag	act	240
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Thr	
65					70					75					80	

003727-942660

acg gtt tat ctg caa atg aac agc ctg aaa cct gaa gat acg gcc gtt 288
 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
 85 90 95

tat tat tgt gcc gct cga ccg gtc cgc gtg gat gat att tcc ctg ccg 336
 Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu Pro
 100 105 110

gtt ggg ttt gac tac tgg ggc cag ggg acc cag gtc acc gtc tcc tca 384
 Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
 115 120 125

gaa caa aaa ctc atc tca gaa gag gat ctg aat taataagggc taagctcgaa 437
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
 130 135

ttc 440

<210> 2

<211> 139

<212> PRT

<213> Artificial

<400> 2

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly His
 20 25 30

Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu Arg
 35 40 45

Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr Lys
 50 55 60

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
 65 70 75 80

Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
 85 90 95

Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu Pro
 100 105 110

Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
 115 120 125

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
 130 135

009737476 "151800

```
<220>
<223>   myc linker
<400>   3
```

```
<210> 4
<211> 471
<212> DNA
<213> Artificial
```

```
<220>
<223>    VHH with linker
<220>
<221>    CDS
<222>    (1)..(459)
```

<400>																4	
cag	gtg	cag	ctg	cag	cag	tca	ggg	gga	ggc	ttg	gtg	cag	gct	ggg	ggg	48	
Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Gly	Gly	Leu	Val	Gln	Ala	Gly	Gly		
1				5				10				15					
tct	ctg	aga	ctc	tcc	tgt	gta	gct	tct	gaa	agc	agc	ttc	agc	aac	aat	96	
Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser	Glu	Ser	Ser	Phe	Ser	Asn	Asn		
			20				25				30						
cac	atg	ggc	tgg	tac	cgc	cgg	gct	cca	ggg	aac	cag	cgc	gag	ctg	gtc	144	
His	Met	Gly	Trp	Tyr	Arg	Arg	Ala	Pro	Gly	Asn	Gln	Arg	Glu	Leu	Val		
			35				40				45						
gca	act	att	agt	cct	ggt	ggt	agc	aca	cac	tat	gta	gac	tcc	gtg	aag	192	
Ala	Thr	Ile	Ser	Pro	Gly	Gly	Ser	Thr	His	Tyr	Val	Asp	Ser	Val	Lys		
			50				55				60						
ggc	cga	ttc	acc	atc	tcc	cga	gac	aac	gcc	aag	aac	aca	gtg	tat	cta	240	
Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Val	Tyr	Leu		
65				70				75				80					
caa	atg	gac	agc	ctg	aaa	cca	gag	gac	acg	gcc	gtc	tat	tac	tgt	gct	288	
Gln	Met	Asp	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala		
			85				90				95						
gcc	aag	ggg	agg	ggg	ctg	cag	gct	atg	cag	tac	tgg	ggc	cag	ggg	acc	336	
Ala	Lys	Gly	Arg	Gly	Leu	Gln	Ala	Met	Gln	Tyr	Trp	Gly	Gln	Gly	Thr		

```
<210> 5
<211> 153
<212> PRT
<213> Artificial
```

```

<400>      5
Gln Val Gln Leu Gln Gln Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 1              5              10              15
Ser Leu Arg Leu Ser Cys Val Ala Ser Glu Ser Ser Phe Ser Asn Asn
      20              25              30
His Met Gly Trp Tyr Arg Arg Ala Pro Gly Asn Gln Arg Glu Leu Val
      35              40              45
Ala Thr Ile Ser Pro Gly Gly Ser Thr His Tyr Val Asp Ser Val Lys
      50              55              60
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65              70              75              80
Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
      85              90              95
Ala Lys Gly Arg Gly Leu Gln Ala Met Gln Tyr Trp Gly Gln Gly Thr
      100              105              110
Leu Val Thr Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala
      115              120              125
Ala Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile
      130              135              140
Ser Glu Glu Asp Leu Asn Gly Ala Ala
145              150

```

```
<220>
<223>    VHH with linker
<220>
<221>    CDS
<222>    (1)..(456)
```

$\langle 210 \rangle$	7
$\langle 211 \rangle$	152

<213> Artificial

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile
20 25 30

Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val
35 40 45

Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80

Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu
100 105 110

```
Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala
      115                      120                      125
```

Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser
130 135 140

Glu Glu Asp Leu Asn Gly Ala Ala
145 150

<211> 462

<212> DNA

<213> Artificial

 $\langle 220 \rangle$

<223> VHH with linker

 $\langle 220 \rangle$

<221> CDS

<222> (1) .. (450)

<400> 8
 acc atg gcc cag gtg aaa ctg cag cag tct ggg gga gga ttg gtg cag 48
 Thr Met Ala Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln
 1 5 10 15

 gct ggg ggc cct ctg agg ctc tcc tgt gca gcc tct gga cgc acc ttc 96
 Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe
 20 25 30

 agt aac tat gcc gtg ggc tgg ttc cgc cag gct cca ggg aag gag cgt 144
 Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg
 35 40 45

 gag ttt gtc gct gct att agc cgt gat ggt ggg cgc aca tac tat gcg 192
 Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala
 50 55 60

 gac tcc gtg aag ggc cga ttc gcc gtc tcc aga gac tac gcc gag aac 240
 Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn
 65 70 75 80

 acg gtg tat ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt 288
 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
 85 90 95

 tat tac tgt aac aca agg gcc tac tgg ggc cag ggg acc cag gtc acc 336
 Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr
 100 105 110

 gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg gcc gcc cat 384
 Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His
 115 120 125

 cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag 432
 His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu
 130 135 140

 gat ctg aat ggg gcc gca tagtaacaat tg 462
 Asp Leu Asn Gly Ala Ala
 145 150

<210> 9

<211> 150

<212> PRT

<213> Artificial

<400> 9

Thr Met Ala Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln
 1 5 10 15

 Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe
 20 25 30

 Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg
 35 40 45

009727 " 92425250

Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala
50 55 60

Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn
65 70 75 80

Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His
115 120 125

His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu
130 135 140

Asp Leu Asn Gly Ala Ala
145 150

<210> 10

<211> 471

<212> DNA

<213> Artificial

<220>

<223> VHH with linker

<220>

<221> CDS

<222> (1)..(459)

<400> 10

acc atg gcc cag gtg aaa ctg cag cag tct ggg gga gga ttg gtg cag 48
Thr Met Ala Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln
1 5 10 15

gct ggg ggc cct ctg agg ctc tcc tgt gca gcc tct gga cgc acc ttc 96
Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe
20 25 30

agt aac tat gcc gtg ggc tgg ttc cgc cag gct cca ggg aag gag cgt 144
Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg
35 40 45

gag ttt gtc gct gct att agc cgt gat ggt ggg cgc aca tac tat gcg 192
Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala
50 55 60

gac tcc gtg aag ggc cga ttc gcc gtc tcc aga gac tac gcc gag aac 240

008747 944660

Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn
 65 70 75 80
 acg gtg tat ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt 288
 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
 85 90 95
 tat tac tgt aac aca agg gcc tac tgg ggc cag ggg acc cag gtc acc 336
 Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr
 100 105 110
 gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg gcc gcc cat 384
 Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His
 115 120 125
 cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag 432
 His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu
 130 135 140
 gat ctg aat agt gag aaa gat gag cta tgataacaat tg 471
 Asp Leu Asn Ser Glu Lys Asp Glu Leu
 145 150
 <210> 11
 <211> 153
 <212> PRT
 <213> Artificial
 <400> 11
 Thr Met Ala Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln
 1 5 10 15
 Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe
 20 25 30
 Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg
 35 40 45
 Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala
 50 55 60
 Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn
 65 70 75 80
 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
 85 90 95
 Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr
 100 105 110
 Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His
 115 120 125

008727 "94466660

His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu
 130 135 140

Asp Leu Asn Ser Glu Lys Asp Glu Leu
 145 150

<210> 12

<211> 38

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 12
 agctgcgata gcaagcttgg taccgggaat tctctaga

38

<210> 13

<211> 42

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 13
 aatttctaga gaattcccg tacciaagctt gcttgcgata gc

42

<210> 14

<211> 31

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 14
 tcgacccatg gcccgctagc caattggagc t

31

<210> 15

<211> 23

<212> DNA

009727 9475 43400

tggaattc

189

<210> 19

<211> 21

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 19

ccggcaacag gattcaatct t

21

<210> 20

<211> 40

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 20

agctccatgg gatttgttct cttttcaciaa ttgccttcac

40

<210> 21

<211> 35

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 21

ttcttcttgt ctctacactt ctcttattcc tagta

35

<210> 22

<211> 35

<212> DNA

<213> Artificial

003427 "944E260

Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala Gln Val
20 25 30

Gln Leu

<210> 29

<211> 21

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 29
gacatcccat ggcaagcatc a

21

<210> 30

<211> 21

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 30
aagcttggtta acagccctta a

21

<210> 31

<211> 21

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 31
agggtgtggtta acaaacttga t

21

<210> 32

<211> 44

<212> DNA

<213> Artificial

003421 92426260

<220>

<223> PCR primer

<400> 32

agactgctgc agctgcacct gctttccaca aacaatggta gctg

44

<210> 33

<211> 19

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 33

aattaaccct cactaaagg

19

<210> 34

<211> 254

<212> DNA

<213> Artificial

<220>

<223> GBSS leader

<220>

<221> CDS

<222> (3)..(254)

<400> 34

cc atg gca agc atc aca gct tca cac cac ttt gtg tca aga agc caa
 Met Ala Ser Ile Thr Ala Ser His His Phe Val Ser Arg Ser Gln
 1 5 10 15

47

act tca cta gac acc aaa tca acc ttg tca cag ata gga ctc agg aac
 Thr Ser Leu Asp Thr Lys Ser Thr Leu Ser Gln Ile Gly Leu Arg Asn
 20 25 30

95

cat act ctg act cac aat ggt tta agg gct gtt aac aaa ctt gat ggg
 His Thr Leu Thr His Asn Gly Leu Arg Ala Val Asn Lys Leu Asp Gly
 35 40 45

143

ctc caa tca aga act aat act aag gta aca ccc aag atg gca tcc aga
 Leu Gln Ser Arg Thr Asn Thr Lys Val Thr Pro Lys Met Ala Ser Arg
 50 55 60

191

act gag acc aag aga cct gga tgc tca gct acc att gtt tgt gga aaa
 Thr Glu Thr Lys Arg Pro Gly Cys Ser Ala Thr Ile Val Cys Gly Lys
 65 70 75

239

008767 " 92426.269

<213> Artificial

<220>

<223> synthetic insert

<400> 37
gctgcacctg

10

<210> 38

<211> 24

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 38
cgcaagaccc ttcctctata taag

24

<210> 39

<211> 60

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 39
gagctcgaat tcttattata gctcatcttt ctctgaattc agatcctctt ctgagatgag

60

<210> 40

<211> 26

<212> PRT

<213> Artificial

<220>

<223> linker

<400> 40

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr.
20 25

<210> 41

<211> 20

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 41
atcctcaact tccaatcaga

20

<210> 42

<211> 19

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 42
ttcttgagag atagcttga

19

<210> 43

<211> 30

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 43
gatcccatgg cccgctagcc aattggagct

30

<210> 44

<211> 22

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 44
ccaattggct agcgggccat gg

22

<210> 45

<211> 29

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 45
gatccacctc gagtgtaaac catggcccg

29

<210> 46

<211> 29

<212> DNA

<213> Artificial

<220>

<223> synthetic insert

<400> 46
ctagcgggcc atgggtttaca ctcgaggtg

29

<210> 47

<211> 20

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 47
attgcctacg gcagccgctg

20

<210> 48

<211> 51

<212> DNA

<213> Artificial

003746 13300

<220>

<223> PCR primer

<400> 48

tccaaccaat tggtactatg cggccccatt cagatcctct tctgagatga g

51

<210> 49

<211> 25

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 49

gtctgtctaa agtaaagtag atgcg

25

<210> 50

<211> 60

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 50

tccaaccaat tggtatcata gtcactcttt ctactattc agatcctctt ctgagatgag

60

<210> 51

<211> 29

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 51

agtccccat ggtacgtcct gtagaaacc

29

<210> 52

<211> 25

<212> DNA

0087 924260

<213> Artificial

<220>

<223> PCR primer

<400> 52

cgttttcgtc ggtaatcacc attcc

25

<210> 53

<211> 24

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 53

cgcaagaccc ttccctttata taag

24

<210> 54

<211> 1154

<212> DNA

<213> Artificial

<220>

<223> HCV33-hinge-CH2-CH3

<220>

<221> CDS

<222> (3)..(1136)

<400> 54

cc atg gag gtg cag ctg cag gag tca ggg gga gga ttg gtg cag gct
Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala
1 5 10 15

47

ggg ggc tct ctg aga ctc tcc tgt gca gcc tcg gga cgc gcc acc agt
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser
20 25 30

95

ggt cat ggt cac tat ggt atg ggc tgg ttc cgc cag gtt cca ggg aag
Gly His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys
35 40 45

143

gag cgt gag ttt gtc gca gct att agg tgg agt ggt aaa gag aca tgg
Glu Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp
50 55 60

191

<213> Artificial

<220>

<223> PCR primer

<400> 52
cgttttcgtc ggtaatcacc attcc

25

<210> 53

<211> 24

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 53
cgcaagaccc ttcctttata taag

24

<210> 54

<211> 1154

<212> DNA

<213> Artificial

<220>

<223> HCV33-hinge-CH2-CH3

<220>

<221> CDS

<222> (3)..(1136)

<400> 54
cc atg gag gtg cag ctg cag gag tca ggg gga gga ttg gtg cag gct 47
Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala
1 5 10 15
ggg ggc tct ctg aga ctc tcc tgt gca gcc tog gga cgc gcc acc agt 95
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser
20 25 30
ggt cat ggt cac tat ggt atg ggc tgg ttc cgc cag gtt cca ggg aag 143
Gly His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys
35 40 45
gag cgt gag ttt gtc gca gct att agg tgg agt ggt aaa gag aca tgg 191
Glu Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp
50 55 60

008746 947660

tat aaa gac tcc gtg aag ggc cga ttc acc atc tcc aga gat aac gcc Tyr Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala 65 70 75	239
aag act acg gtt tat ctg caa atg aac agc ctg aaa cct gaa gat acg Lys Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr 80 85 90 95	287
gcc gtt tat tat tgt gcc gct cga ccg gtc cgc gtg gat gat att tcc Ala Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser 100 105 110	335
ctg ccg gtt ggg ttt gac tac tgg ggc cag ggg acc cag gtc acc gtc Leu Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val 115 120 125	383
tcc tca gaa ccc aag aca cca aaa cca caa cca caa cca caa cca caa Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln 130 135 140	431
cca caa ccc aat cct aca aca gaa tcc aag tgt ccc aaa tgt cca gcc Pro Gln Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala 145 150 155	479
cct gag ctc ctg gga ggg ccc tca gtc ttc atc ttc ccc ccg aaa ccc Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro 160 165 170 175	527
aag gac gtc ctc tcc att tct ggg agg ccc gag gtc acg tgc gtt gtg Lys Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val 180 185 190	575
gta gac gtg ggc cag gaa gac ccc gag gtc agt ttc aac tgg tac att Val Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile 195 200 205	623
gat ggc gca gag gtg cga acg gcc aac acg agg cca aaa gag gaa cag Asp Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln 210 215 220	671
ttc aac agc acg tac cgc gtg gtc agc gtc ctg ccc atc cag cac cag Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln 225 230 235	719
gac tgg ctg acg ggg aaa gag ttc aaa tgc aag gtc aac aac aaa gct Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala 240 245 250 255	767
ctc ccg gcc ccc atc gag aag acc atc tcc aag gcc aaa ggg cag acc Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr 260 265 270	815
cgg gag ccg cag gtg tac gcc ctg gcc cca cac cgg gaa gag ctg gcc Arg Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala 275 280 285	863
aag gac acc gtg agc gta acc tgc ctg gtc aaa ggc ttc tac cca cct Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro 290 295 300	911
gat atc aac gtt gag tgg cag agg aac ggt cag ccg gag tca gag ggc Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly 305 310 315	959
acc tac gcc acc acg cca ccc cag ctg gac aac gac ggg acc tac ttc Thr Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe 320 325 330 335	1007

003727 92426260

ctc tac agc aag ctc tcg gtg gga aag aac acg tgg cag cgg gga gaa 1055
 Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu
 340 345 350

acc ttc acc tgt gtg gtg atg cac gag gcc ctg cac aac cac tac acc 1103
 Thr Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr
 355 360 365

cag aaa tcc atc acc cag tct tcg ggt aaa taa taagaattcg agctcgaa 1154
 Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys
 370 375

<210> 55

<211> 377

<212> PRT

<213> Artificial

<400> 55

Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly
 1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly
 20 25 30

His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu
 35 40 45

Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr
 50 55 60

Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
 65 70 75 80

Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala
 85 90 95

Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu
 100 105 110

Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser
 115 120 125

Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln Pro
 130 135 140

Gln Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala Pro
 145 150 155 160

Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys
 165 170 175

008727" 9242E260

Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val
 180 185 190

Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile Asp
 195 200 205

Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln Phe
 210 215 220

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp
 225 230 235 240

Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu
 245 250 255

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg
 260 265 270

Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala Lys
 275 280 285

Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp
 290 295 300

Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr
 305 310 315 320

Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu
 325 330 335

Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu Thr
 340 345 350

Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 355 360 365

Lys Ser Ile Thr Gln Ser Ser Gly Lys
 370 375

<210> 56

<211> 1172

<212> DNA

<213> Artificial

<220>

<223> hinge-HCV33-CH2-CH3-SEKDEL

003461924260

<222> (3) .. (1154)

<400>	56																
cc atg gag gtg cag ctg cag gag tca ggg gga gga ttg gtg cag gct																	47
Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala																	
1					5				10				15				
ggg ggc tct ctg aga ctc tcc tgt gca gcc tcg gga cgc gcc acc agt																	95
Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser																	
					20				25				30				
ggt cat ggt cac tat ggt atg ggc tgg ttc cgc cag gtt cca ggg aag																	143
Gly His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys																	
					35				40				45				
gag cgt gag ttt gtc gca gct att agg tgg agt ggt aaa gag aca tgg																	191
Glu Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp																	
									55				60				
tat aaa gac tcc gtg aag ggc cga ttc acc atc tcc aga gat aac gcc																	239
Tyr Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala																	
	65								70				75				
aag act acg gtt tat ctg caa atg aac agc ctg aaa cct gaa gat acg																	287
Lys Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr																	
80					85				90				95				
gcc gtt tat tat tgt gcc gct cga ccg gtc cgc gtg gat gat att tcc																	335
Ala Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser																	
					100				105				110				
ctg ccg gtt ggg ttt gac tac tgg ggc cag ggg acc cag gtc acc gtc																	383
Leu Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val																	
					115				120				125				
tcc tca gaa ccc aag aca cca aaa cca caa cca caa cca caa cca cca																	431
Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln																	
	130								135				140				
cca caa ccc aat cct aca aca gaa tcc aag tgt ccc aaa tgt cca gcc																	479
Pro Gln Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala																	
	145				150				155								
cct gag ctc ctg gga ggg ccc tca gtc ttc atc ttc ccc ccg aaa ccc																	527
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro																	
160					165				170				175				
aag gac gtc ctc tcc att tct ggg agg ccc gag gtc acg tgc gtt gtg																	575
Lys Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val																	
					180				185				190				
gta gac gtg ggc cag gaa gac ccc gag gtc agt ttc aac tgg tac att																	623
Val Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile																	
					195				200				205				
gat ggc gca gag gtg cga acg gcc aac acg agg cca aaa gag gaa cag																	671
Asp Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln																	
	210								215				220				
ttc aac agc acg tac cgc gtg gtc agc gtc ctg ccc atc cag cac cag																	719
Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln																	
	225				230				235								

gac tgg ctg acg ggg aaa gag ttc aaa tgc aag gtc aac aac aaa gct 767
 Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala
 240 245 250 255

ctc ccg gcc ccc atc gag aag acc atc tcc aag gcc aaa ggg cag acc 815
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr
 260 265 270

cgg gag ccg cag gtg tac gcc ctg gcc cca cac cgg gaa gag ctg gcc 863
 Arg Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala
 275 280 285

aag gac acc gtg agc gta acc tgc ctg gtc aaa ggc ttc tac cca cct 911
 Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro
 290 295 300

gat atc aac gtt gag tgg cag agg aac ggt cag ccg gag tca gag ggc 959
 Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly
 305 310 315

acc tac gcc acc acg cca ccc cag ctg gac aac gac ggg acc tac ttc 1007
 Thr Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe
 320 325 330 335

ctc tac agc aag ctc tcg gtg gga aag aac acg tgg cag cgg gga gaa 1055
 Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Arg Gly Glu
 340 345 350

acc ttc acc tgt gtg gtg atg cac gag gcc ctg cac aac cac tac acc 1103
 Thr Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr
 355 360 365

cag aaa tcc atc acc cag tct tcg ggt aaa tct gag aaa gat gag cta 1151
 Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys Ser Glu Lys Asp Glu Leu
 370 375 380

taa taagaattcg agctcgaa 1172

<210> 57

<211> 383

<212> PRT

<213> Artificial

<400> 57

Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly
 1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly
 20 25 30

His Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu
 35 40 45

Arg Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr
 50 55 60

09737476 "131300

Lys Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
 65 70 75 80
 Thr Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala
 85 90 95
 Val Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu
 100 105 110
 Pro Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser
 115 120 125
 Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln Pro Gln Pro
 130 135 140
 Gln Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala Pro
 145 150 155 160
 Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys
 165 170 175
 Asp Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val
 180 185 190
 Asp Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile Asp
 195 200 205
 Gly Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln Phe
 210 215 220
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp
 225 230 235 240
 Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu
 245 250 255
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg
 260 265 270
 Glu Pro Gln Val Tyr Ala Leu Ala Pro His Arg Glu Glu Leu Ala Lys
 275 280 285
 Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp
 290 295 300
 Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr
 305 310 315 320
 Tyr Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu
 325 330 335

09737476 121800

<211> 42

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 61

ttcgagctcg aattcttatt atttaccga agactgggtg at

42

<210> 62

<211> 27

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 62

ctgaggagac ggtgacctgg gtccct

27

<210> 63

<211> 46

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 63

agcccctgag ctctctggag ggccctcagt ctcatcttc cccccc

46

<210> 64

<211> 61

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 64

ttcgagctcg aattcttatt atttaccga agactgggtg atggatttct ggggtgtagtg

60

008727 924260

g

61

<210> 65

<211> 79

<212> DNA

<213> Artificial

<220>

<223> PCR primer

<400> 65

ttcgagctcg aattcttatt atagctcatc tttctcagat ttacccgaag actgggtgat 60

ggatttctgg gtgtagtg 79

<210> 66

<211> 461

<212> DNA

<213> Artificial

<220>

<223> VHH with linker

<220>

<221> CDS

<222> (3) .. (449)

<400> 66

cc atg gcc cag gtg cag ctg cag gag tct ggg gga ggc ttg gtg cag 47

Met Ala Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln

1 5 10 15

gct ggg ggg tct ctg agg ctc tcc tgt gca gcc tct gga agc att ttc 95

Ala Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe

20 25 30

aga cgt ccg cat atg ggt tgg ttc cgc cag gct cca ggg cag gag cgc 143

Arg Arg Pro His Met Gly Trp Phe Arg Gln Ala Pro Gly Gln Glu Arg

35 40 45

gag ttg gtc gca ctg att tct gcg ggt ggt cgt aca tgg tat gca gac 191

Glu Leu Val Ala Leu Ile Ser Ala Gly Gly Arg Thr Trp Tyr Ala Asp

50 55 60

tcc gtg aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac acg 239

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr

65 70 75

ctg tat ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt tat 287

003431300946260

Leu Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr
80 85 90 95

tac tgt act gcc ggg ggt tcg tac tgg ggc cag ggg acc cag gtc acc 335
Tyr Cys Thr Ala Gly Gly Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

gtc gcc tca gaa ccc aag aca cca aaa cca caa cca gcg gcc gcc cat 383
Val Ala Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala Ala His
115 120 125

cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag 431
His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu
130 135 140

gat ctg aat ggg gcc gca tagtaacaat tg 461
Asp Leu Asn Gly Ala Ala
145

<210> 67

<211> 149

<212> PRT

<213> Artificial

<400> 67

Met Ala Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala
1 5 10 15

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Phe Arg
20 25 30

Arg Pro His Met Gly Trp Phe Arg Gln Ala Pro Gly Gln Glu Arg Glu
35 40 45

Leu Val Ala Leu Ile Ser Ala Gly Gly Arg Thr Trp Tyr Ala Asp Ser
50 55 60

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu
65 70 75 80

Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Thr Ala Gly Gly Ser Tyr Trp Gly Gln Gly Thr Gln Val Thr Val
100 105 110

Ala Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala Ala His His
115 120 125

His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp
130 135 140

00346260

Leu Asn Gly Ala Ala
145

09737475 121800

Parameter	Value	Unit
Initial concentration	1.0	g/L
Initial pH	7.0	
Temperature	25	°C
Time	0, 1, 2, 4, 8, 16, 32, 64, 128, 256, 512, 1024, 2048, 4096, 8192, 16384, 32768, 65536, 131072, 262144, 524288, 1048576, 2097152, 4194304, 8388608, 16777216, 33554432, 67108864, 134217728, 268435456, 536870912, 1073741824, 2147483648, 4294967296, 8589934592, 17179869184, 34359738368, 68719476736, 137438953472, 274877906944, 549755813888, 1099511627776, 2199023255552, 4398046511104, 8796093022208, 17592186044416, 35184372088832, 70368744177664, 140737488355328, 281474976710656, 562949953421312, 1125899906842624, 2251799813685248, 4503599627370496, 9007199254740992, 18014398509481984, 36028797018963968, 72057594037927936, 144115188075855872, 288230376151711744, 576460752303423488, 1152921504606846976, 2305843009213693952, 4611686018427387904, 9223372036854775808, 18446744073709551616, 36893488147419103232, 73786976294838206464, 147573952589676412928, 295147905179352825856, 590295810358705651712, 1180591620717411303424, 2361183241434822606848, 4722366482869645213696, 9444732965739290427392, 18889465931478580854784, 37778931862957161709568, 75557863725914323419136, 151115727451828646838272, 302231454903657293676544, 604462909807314587353088, 1208925819614629174706176, 2417851639229258349412352, 4835703278458516698824704, 9671406556917033397649408, 19342813113834066795298816, 38685626227668133590597632, 77371252455336267181195264, 154742504910672534362390528, 309485009821345068724781056, 618970019642690137449562112, 1237940039285380274899124224, 2475880078570760549798248448, 4951760157141521099596496896, 9903520314283042199192993792, 19807040628566084398385987584, 39614081257132168796771975168, 79228162514264337593543950336, 158456325028528675187087900672, 316912650057057350374175801344, 633825300114114700748351602688, 1267650600228229401496703205376, 2535301200456458802993406410752, 5070602400912917605986812821504, 10141204801825835211973625643008, 20282409603651670423947251286016, 40564819207303340847894502572032, 81129638414606681695789005144064, 162259276829213363391578010288128, 324518553658426726783156020576256, 649037107316853453566312041152512, 1298074214633706907132624082305024, 2596148429267413814265248164610048, 5192296858534827628530496329220096, 10384593717069655257060992658440192, 20769187434139310514121985316880384, 41538374868278621028243970633760768, 83076749736557242056487941267521536, 166153499473114484112975882535043072, 332306998946228968225951765070086144, 664613997892457936451903530140172288, 1329227995784915872903807060280344576, 2658455991569831745807614120560689152, 5316911983139663491615228241121378304, 10633823966279326983230456482242756608, 21267647932558653966460912964485513216, 42535295865117307932921825928971026432, 85070591730234615865843651857942052864, 170141183460469231731687303715884105728, 340282366920938463463374607431768211456, 680564733841876926926749214863536422912, 1361129467683753853853498429727072845824, 2722258935367507707706996859454145691648, 5444517870735015415413993718908291383296, 10889035741470030830827987437816582766592, 21778071482940061661655974875633165533184, 43556142965880123323311949751266331066368, 87112285931760246646623899502532662132736, 174224571863520493293247799005065324265472, 348449143727040986586495598010130648530944, 696898287454081973172991196020261297061888, 1393796574908163946345982392040522594123776, 2787593149816327892691964784081045188247552, 5575186299632655785383929568162090376495104, 11150372599265311570767859136324180752990208, 22300745198530623141535718272648361505980416, 44601490397061246283071436545296723011960832, 89202980794122492566142873090593446023921664, 178405961588244985132285746181186892047843328, 356811923176489970264571492362373784095686656, 713623846352979940529142984724747568191373312, 1427247692705959881058285969449495136382746624, 2854495385411919762116571938898990272765493248, 5708990770823839524233143877797980545530986496, 11417981541647679048466287755595961091061972992, 2283596308329	

SN 09-737-476 Mail Date 12-18-00

- ☐ Non-English Specification
- ☒ Specification contains drawing(s) on page(s) _____ or table(s) 57-59
- ☐ Landscape orientation of text ☐ Specification ☐ Claims ☐ Abstract
- ☐ Handwritten ☐ Specification ☐ Claims ☐ Abstract
- ☐ More than one column ☐ Specification ☐ Claims ☐ Abstract
- ☐ Improper line spacing ☐ Specification ☐ Claims ☐ Abstract
- ☐ Claims not on separate page(s)
- ☐ Abstract not on separate page(s)
- ☐ Improper paper size -- Must be either A4 (21 cm x 29.7 cm) or 8-1/2" x 11"
- ☐ Specification page(s) _____ ☐ Abstract
- ☐ Drawing page(s) _____ ☐ Claim(s)
- ☐ Improper margins
- ☐ Specification page(s) _____ ☐ Abstract
- ☐ Drawing page(s) _____ ☐ Claim(s)
- ☐ Not reproducible
- | <u>Reason</u> | <u>Section</u> |
|---|--|
| <input type="checkbox"/> Paper too thin | <input type="checkbox"/> Specification page(s) _____ |
| <input type="checkbox"/> Glossy pages | <input type="checkbox"/> Drawing page(s) _____ |
| <input type="checkbox"/> Non-white background | <input type="checkbox"/> Abstract |
| | <input type="checkbox"/> Claim(s) |
- ☐ Drawing objection(s)
- ☐ Missing lead lines, drawing(s) _____
- ☐ Line quality is too light, drawing(s) _____
- ☐ More than 1 drawing and not numbered correctly
- ☐ Non-English text, drawing(s) _____
- ☐ Excessive text, drawing(s) _____
- ☐ Photographs capable of illustration, drawing(s) _____

United States Patent & Trademark Office
Office of Initial Patent Examination -- Scanning Division



Application deficiencies found during scanning:

☐ Page(s) _____ of _____ were not present
for scanning. (Document title)

☐ Page(s) _____ of _____ were not present
for scanning. (Document title)

☐ *Scanned copy is best available.*

FILED ALSO 23 sheets of drawing